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**AMENDMENTS TO THE CLAIMS**

The claims are not amended. A complete listing of the claims, including their current status, is set forth below.

1. (Previously presented) A method of identifying a region of a genome of a cell to which a protein of interest binds, comprising the steps of:

- a) crosslinking DNA binding protein in the cell to genomic DNA of the cell, thereby producing DNA binding protein crosslinked to genomic DNA;
- b) generating DNA fragments of the genomic DNA crosslinked to DNA binding protein in a) by sonication, thereby producing a mixture comprising DNA fragments to which DNA binding protein is bound;
- c) removing a DNA fragment to which the protein of interest is bound from a first portion of the mixture produced in b);
- d) separating the DNA fragment of c) from the protein of interest;
- e) labeling the DNA fragment of d) with a first fluorescent label by:
  - i. blunting said DNA fragment to produce blunt ends;
  - ii. ligating adaptors to said blunt ends;
  - iii. amplifying said DNA fragment using a primer that binds to said adaptors; and
  - iv. labeling said DNA fragment either during or after said amplifying to produce a labeled DNA fragment;
- f) labeling a second portion of the mixture produced in b) with a second fluorescent label by:
  - i. blunting said second portion to produce a blunted sample;
  - ii. ligating adaptors to said blunted sample;
  - iii. amplifying said blunted sample using a primer that binds to said adaptors; and
  - iv. labeling said blunted sample either during or after said amplifying to produce a second sample;
- g) combining the labeled DNA fragment of e) and the second sample of f) with a DNA microarray comprising sequences that detect

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intergenic regions, under conditions in which nucleic acid hybridization occurs;  
and

h) comparing results obtained from said first fluorescent label to results obtained from said second fluorescent label to identify a sequence of g) to which the DNA fragment hybridizes,

whereby the sequence identified in h) indicates the region of the genome in the cell to which the protein of interest binds.

2. (Original) The method of Claim 1 wherein the cell is a eukaryotic cell.
3. (Original) The method of Claim 1 wherein the protein of interest is selected from the group consisting of: a transcription factor and an oncogene.
4. (Original) The method of Claim 1 wherein the DNA binding protein of the cell is crosslinked to the genome of the cell using formaldehyde.
5. (Original) The method of Claim 1 wherein the DNA fragment of c) to which is bound the protein of interest is identified using an antibody which binds to the protein of interest.
6. (Original) The method of Claim 1 wherein the DNA fragment of e) is amplified using ligation-mediated polymerase chain reaction.
7. (Canceled)
8. (Previously Presented) The method of Claim 1 further comprising:  
h) comparing the sequences identified in g) with a control.
9. - 14. (Canceled)
15. (Previously Presented) The method of Claim 1 wherein after the DNA fragment is separated from the protein of interest, the DNA fragment is labeled with a fluorescent dye.

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16. (Previously Presented) The method of Claim 15 wherein the fluorescent dye is selected from the group consisting of: Cy5 and Cy3.

17. (Previously Presented) The method of Claim 1 wherein the DNA fragments are generated using shearing conditions.

18.-86 (Cancelled)

87. (Previously presented) The method of Claim 1 further comprising:  
(i) identifying a DNA binding site of the protein of interest in the sequence identified in (h) wherein the protein of interest is a transcription factor.

88. (Previously Presented) The method of Claim 1, wherein said sequences are across a chromosome and the chromosome is examined to determine where the protein of interest binds.

89. (Cancelled)

90. (Previously Presented) The method of Claim 1, wherein said amplifying comprises non-specifically amplifying.

91. (Previously Presented) The method according to Claim 90, wherein said non-specifically amplifying is by ligation-mediated polymerase chain reaction (LM-PCR).

92. (Previously Presented) The method according to Claim 1, wherein said array contains spots representing all of the genome of said cell.